

# SEQUENCE LISTING

<110> Harrington, et al.

<120> Mammalian Flap Specific-Endonuclease

<130> 9584-017

<140> 09/586,744

<141> 2000-06-02

<160> 74

<170> PatentIn version 3.0

<210> 1

<211> 380

<212> PRT

<213> Homo sapiens

<400> 1

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Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser His Leu
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Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu

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<212> DNA

<213> Homo sapiens

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<213> Mus musculus

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Tyr Val Phe Asp Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu Leu Ala  
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180 185 190  
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195 200 205  
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210 215 220  
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225 230 235 240  
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Val Arg Arg Leu Asp Pro Ser Lys Tyr Pro Val Pro Glu Asn Trp Leu  
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<212> PRT

<213> *Saccharomyces cerevisiae*

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Ile Asp Ala Ser Met Ser Leu Tyr Gln Phe Leu Ile Ala Val Arg Gln
35           40           45

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<211> 386

<212> PRT

<213> *Saccharomyces cerevisiae*

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Asn	Leu	Lys	Asn	Phe	Lys	Asp	Trp	Tyr	Asn	Asn	Gly	Gln	Phe	Asp	Lys	
			245						250					255		

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 Thr Gln Leu Gly Trp Pro His Glu Lys Ser Asp Glu Ile Leu Ile Pro  
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 Ile Asn Glu Phe Phe Pro Arg Glu Tyr Ile Ser Gly Asp Lys Lys Leu  
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<212> DNA

<213> *Saccharomyces cerevisiae*

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cgt acc atg cgc atg gag aat ggc atc aag cct gtg tac gtc ttt gat	355
Arg Thr Met Arg Met Glu Asn Gly Ile Lys Pro Val Tyr Val Phe Asp	
70 75 80	
ggc aaa cca cca cag ctg aag tca ggc gag ctg gcc aag cgc agt gag	403
Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu Leu Ala Lys Arg Ser Glu	
85 90 95 100	
agg cgc gcc gag gct gag aag caa ctg cag cag gct cag cag gct ggg	451
Arg Arg Ala Glu Ala Glu Lys Gln Leu Gln Gln Ala Gln Gln Ala Gly	
105 110 115	
atg gag gag gag gtg gag aag ttc acc aag agg ctc gtg aag gtc acc	499
Met Glu Glu Glu Val Glu Lys Phe Thr Lys Arg Leu Val Lys Val Thr	
120 125 130	
aag caa cac aat gat gag tgc aaa cac ctg ctg agc ctc atg ggc atc	547
Lys Gln His Asn Asp Glu Cys Lys His Leu Leu Ser Leu Met Gly Ile	
135 140 145	
cct tac ctt gat gca ccc agc gag gca gag gcc agc tgt gct gcc ctg	595
Pro Tyr Leu Asp Ala Pro Ser Glu Ala Glu Ala Ser Cys Ala Ala Leu	
150 155 160	
gca aag gct ggc aaa gtc tat gct gcg gcc acg gag gac atg gac tgc	643
Ala Lys Ala Gly Lys Val Tyr Ala Ala Ala Thr Glu Asp Met Asp Cys	
165 170 175 180	
ctc act ttt ggc agc ccc gtg cta atg cga cac tta act gcc agt gag	691
Leu Thr Phe Gly Ser Pro Val Leu Met Arg His Leu Thr Ala Ser Glu	
185 190 195	
gcc aag aag ctg ccc atc caa gag ttc cat ctg agc cgc gtc ctg cag	739
Ala Lys Lys Leu Pro Ile Gln Glu Phe His Leu Ser Arg Val Leu Gln	
200 205 210	
gag ctg ggt ctg aac cag gag cag ttt gtg gat ctg tgc atc ctg ctg	787
Glu Leu Gly Leu Asn Gln Glu Gln Phe Val Asp Leu Cys Ile Leu Leu	
215 220 225	
ggt agc gac tac tgc gag agc atc cgt ggc att ggc gcc aag cgg gct	835
Gly Ser Asp Tyr Cys Glu Ser Ile Arg Gly Ile Gly Ala Lys Arg Ala	
230 235 240	
gtg gat ctc atc cag aaa cat aag agc atc gag gag atc gtg agg cgg	883
Val Asp Leu Ile Gln Lys His Lys Ser Ile Glu Glu Ile Val Arg Arg	
245 250 255 260	
ctg gac ccc agc aag tac ccc gtt cca gag aac tgg ctc cac aag gaa	931
Leu Asp Pro Ser Lys Tyr Pro Val Pro Glu Asn Trp Leu His Lys Glu	
265 270 275	
gcc cag cag ctc ttc ctg gag cca gaa gta gtg gac cca gag tct gtg	979
Ala Gln Gln Leu Phe Leu Glu Pro Glu Val Val Asp Pro Glu Ser Val	

280	285	290	
gag ctg aag tgg agc gag cca aat gaa gaa gag ttg gtc aaa ttt atg			1027
Glu Leu Lys Trp Ser Glu Pro Asn Glu Glu Glu Leu Val Lys Phe Met			
295	300	305	
tgt ggt gaa aag cag ttt ttt gaa gag cga att cgc agt ggg gtc aag			1075
Cys Gly Glu Lys Gln Phe Phe Glu Glu Arg Ile Arg Ser Gly Val Lys			
310	315	320	
cgg ctg agt aag agc cgc cag ggc agc acc cag gga cgc ctc gat gat			1123
Arg Leu Ser Lys Ser Arg Gln Gly Ser Thr Gln Gly Arg Leu Asp Asp			
325	330	335	340
ttc ttc aag gtg aca ggc tca ctc tcc tca gct aag cgc aag gag cca			1171
Phe Phe Lys Val Thr Gly Ser Leu Ser Ser Ala Lys Arg Lys Glu Pro			
345	350	355	
gaa ccc aag ggg cct gct aag aag aaa gca aag act ggg gga gcg ggg			1219
Glu Pro Lys Gly Pro Ala Lys Lys Lys Ala Lys Thr Gly Gly Ala Gly			
360	365	370	
aag ttc cga agg gga aaa taaacctgtc cttccccctcc actgtccttg			1267
Lys Phe Arg Arg Gly Lys			
375			
accccaggct gtctatctgt tttgtaccct cggctgcagc acatccctct tgtccctcgt			1327
cttgaggaga gttcattgct tccagcgctg cccttcagag ctttccctct cttgaccctg			1387
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ggcaaaggca ttaagtgtgc cactgacctg tgccctccaag tgatgttctg acagccttcc			1927
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1 5 10 15

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Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln  
35 40 45

Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser Leu Met  
50 55 60

Gly Met Phe Tyr Arg Thr Met Arg Met Glu Asn Gly Ile Lys Pro Val  
65 70 75 80

Tyr Val Phe Asp Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu Leu Ala  
85 90 95

Lys Arg Ser Glu Arg Arg Ala Glu Ala Glu Lys Gln Leu Gln Gln Ala  
100 105 110

Gln Gln Ala Gly Met Glu Glu Glu Val Glu Lys Phe Thr Lys Arg Leu  
115 120 125

Val Lys Val Thr Lys Gln His Asn Asp Glu Cys Lys His Leu Leu Ser  
130 135 140

Leu Met Gly Ile Pro Tyr Leu Asp Ala Pro Ser Glu Ala Glu Ala Ser  
145 150 155 160

Cys Ala Ala Leu Ala Lys Ala Gly Lys Val Tyr Ala Ala Ala Thr Glu  
165 170 175

Asp Met Asp Cys Leu Thr Phe Gly Ser Pro Val Leu Met Arg His Leu  
180 185 190

Thr Ala Ser Glu Ala Lys Lys Leu Pro Ile Gln Glu Phe His Leu Ser  
195 200 205

Arg Val Leu Gln Glu Leu Gly Leu Asn Gln Glu Gln Phe Val Asp Leu  
 210 215 220  
 Cys Ile Leu Leu Gly Ser Asp Tyr Cys Glu Ser Ile Arg Gly Ile Gly  
 225 230 235 240  
 Ala Lys Arg Ala Val Asp Leu Ile Gln Lys His Lys Ser Ile Glu Glu  
 245 250 255  
 Ile Val Arg Arg Leu Asp Pro Ser Lys Tyr Pro Val Pro Glu Asn Trp  
 260 265 270  
 Leu His Lys Glu Ala Gln Gln Leu Phe Leu Glu Pro Glu Val Val Asp  
 275 280 285  
 Pro Glu Ser Val Glu Leu Lys Trp Ser Glu Pro Asn Glu Glu Glu Leu  
 290 295 300  
 Val Lys Phe Met Cys Gly Glu Lys Gln Phe Phe Glu Glu Arg Ile Arg  
 305 310 315 320  
 Ser Gly Val Lys Arg Leu Ser Lys Ser Arg Gln Gly Ser Thr Gln Gly  
 325 330 335  
 Arg Leu Asp Asp Phe Phe Lys Val Thr Gly Ser Leu Ser Ser Ala Lys  
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28

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Arg Glu Asn Asp Ile Lys  
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<213> Homo sapiens

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1 5 10 15

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<211> 22

<212> PRT

<213> Homo sapiens

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Asn Gly Ile Lys Pro Val  
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<211> 24

<212> PRT

<213> Homo sapiens

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Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu Leu Ala Lys Arg Ser Glu  
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<213> Homo sapiens

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Glu Gln Glu Val Glu Lys Phe Thr Lys Arg Leu Val Lys Val Thr Lys  
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Gln His Asn Asp  
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<211> 25

<212> PRT

<213> Homo sapiens

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Glu Ala Ser Cys Ala Ala Leu Val Lys  
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<211> 23

<212> PRT

<213> Homo sapiens

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1 5 10 15

Ala Lys Lys Leu Pro Ile Gln  
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<210> 22

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<213> Homo sapiens

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Ile Leu Gln Glu Leu Gly Leu Asn Gln Glu Gln Phe Val Asp Leu Cys  
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Ile Leu Leu Gly Ser  
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<212> PRT

<213> Homo sapiens

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Arg Gly Ile Gly Pro Lys Arg Ala Val Asp Leu Ile Gln Lys His Lys  
1 5 10 15

Ser Ile Glu Glu Ile Val Arg Arg  
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<210> 24

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<212> PRT

<213> Homo sapiens

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Pro Glu Asn Trp Leu His Lys Glu Ala His Gln Leu Phe Leu Glu Pro  
1 5 10 15

Glu Val Leu Asp  
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<213> Homo sapiens

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Trp Ser Glu Pro Asn Glu Glu Glu Leu Ile Lys Phe Met Cys Gly Glu

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Lys Gln Phe Ser Glu Glu  
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<213> Homo sapiens

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Ser Lys Ser Arg Gln Gly Ser Thr Gln Gly Arg Leu Asp Asp Phe Phe  
1                    5                    10                    15

Lys Val Thr Gly Ser Leu  
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cagttcctga ttgctgttcg ccagggtggg gatgtgctgc agaatgagga gggtagagacc 180

accagccacc tgatgggcat gttctaccgc accattcgca tgatggagaa cggcatcaag 240

cccgtgtatg tctttgatgg caagccgcca cagctcaagt caggcgagct ggccaaacgc 300

agtgagcggc gggctgaggc agagaagcag ctgcagcagg ctcaggctgc tggggccgag	360
caggaggttg aaaaattcac taagcggctg gtgaagggtca ctaagcagca caatgatgag	420
tgcaaacatc tgctgagcct catgggcac ccttatcttg atgcacccag tgaggcagag	480
gccagctgtg ctgccctggg gaaggctggc aaagtctatg ctgcgggtac cgaggacatg	540
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aagctgccaa tccaggaatt ccacctgagc cggattctgc aggagctggg cctgaaccag	660
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<211> 35

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<213> Homo sapiens

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